

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/031,331C
Source: IFW16
Date Processed by STIC: 12/21/04

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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/031,331C

DATE: 12/21/2004

TIME: 14:42:39

Input Set : A:\yamada sequence listing.txt
 Output Set: N:\CRF4\12212004\J031331C.raw

3 <110> APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
 5 <120> TITLE OF INVENTION: Screening of genes to give tolerance against
 6 environmental stress and the applications
 8 <130> FILE REFERENCE: YG12-12PCT

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/031,331C

C--> 11 <141> CURRENT FILING DATE: 2002-01-18

13 <150> PRIOR APPLICATION NUMBER: JP P1999-235910

14 <151> PRIOR FILING DATE: 1999-07-19

16 <150> PRIOR APPLICATION NUMBER: JP P2000-85377

17 <151> PRIOR FILING DATE: 2000-03-24

19 <160> NUMBER OF SEQ ID NOS: 72

21 <170> SOFTWARE: PatentIn Ver. 2.1

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 1018

25 <212> TYPE: DNA

26 <213> ORGANISM: Bruguiera sexangula

28 <220> FEATURE:

29 <221> NAME/KEY: CDS

30 <222> LOCATION: (42)..(464)

32 <400> SEQUENCE: 1

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 34 Met Ala Leu Ser Ser 1 5

35 10 15 20 104
 37 tct gct ctg aga acc gtc tct tct gtg aag gtg gtc ggc cct gca Ser Ala Leu Arg Thr Val Ser Ser Val Lys Val Val Gly Pro Ala

38 10 15 20 104
 41 aga tca aag agt gct act gta ccc acc caa aca gta ttg cct ttc aag 152
 42 Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr Val Leu Pro Phe Lys

43 25 30 35 152
 45 ttc aca aac ccg tcg tta ctc act cga tcg cta agc ttt tca tca aaa 200
 46 Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu Ser Phe Ser Ser Lys

47 40 45 50 200
 49 ggt tca agc ttt gac agc ttc tct gta ccc aaa aga tct ttt tct tgc 248
 50 Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys Arg Ser Phe Ser Cys

51 55 60 65 248
 53 aga agc caa gcc act cca tct gat gat gcc tca aga ccc acc aaa gtt 296
 54 Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser Arg Pro Thr Lys Val

55 70 75 80 85 296
 57 caa gag ctg tgt gtg tat gag atg aac gag aga gat cgt gga agc cct 344
 58 Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg Asp Arg Gly Ser Pro

59 90 95 100 344
 61 gct gtt ctc cgg ttg agc cag aaa cct gtt aat tct ctc ggc gat ctc 392
 62 Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn Ser Leu Gly Asp Leu

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63           105           110           115
65 gtg cct ttc agt aac aaa gtt tac agc gga gac ctg cag aag cga att  440
66 Val Pro Phe Ser Asn Lys Val Tyr Ser Gly Asp Leu Gln Lys Arg Ile
67           120           125           130
69 gga gta acc gca gaa tat gca tcc tgatccaaaa caagccagaa aaaaagggtg  494
70 Gly Val Thr Ala Glu Tyr Ala Ser
71           135           140
73 atcgcttga agcgatatac agctttatt tcgggtggcta tggcacatt gctgtcaag 554
75 ggcataactt gacctacgag gacacgcacc ttgctgtgac gggcggtcg ggcataattt 614
77 aaggagtgtc tggtcaggtt aagctcgac aactcgtgta cccttcaag ctcttctaca 674
79 ctttctactt gcgaggcatc aaggacttgc cgaggagct tacgaagaag cccgttgagc 734
81 cccacccttc tggtagccg atgccgcgg ccaaggctt cgaggccat gccgttgg 794
83 ctaatttac acgttgtga ttaattgtcc ttttgggtt cggatgaact tgagtttagct 854
85 tacagttgca caacgttatg gcgcgagaca cgagagggaa ccttagccat aagaaaatta 914
87 ataatctac ggtgcttta ttttatttct tctatttagtt gaatcgtaa tgaaagtgg 974
89 ccaaattggc tggtagccat tttaaaaaaaa aaaaaaaaaa aaaa 1018
92 <210> SEQ ID NO: 2
93 <211> LENGTH: 141
94 <212> TYPE: PRT
95 <213> ORGANISM: Bruguiera sexangula
97 <400> SEQUENCE: 2
98 Met Ala Leu Ser Ser Ser Ala Leu Arg Thr Val Ser Ser Val Lys
99   1           5           10           15
101 Val Val Gly Pro Ala Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr
102           20           25           30
104 Val Leu Pro Phe Lys Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu
105           35           40           45
107 Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys
108           50           55           60
110 Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser
111   65           70           75           80
113 Arg Pro Thr Lys Val Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg
114           85           90           95
116 Asp Arg Gly Ser Pro Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn
117           100          105          110
119 Ser Leu Gly Asp Leu Val Pro Phe Ser Asn Lys Val Tyr Ser Gly Asp
120           115          120          125
122 Leu Gln Lys Arg Ile Gly Val Thr Ala Glu Tyr Ala Ser
123           130          135          140
127 <210> SEQ ID NO: 3
128 <211> LENGTH: 2060
129 <212> TYPE: DNA
130 <213> ORGANISM: Bruguiera sexangula
132 <220> FEATURE:
133 <221> NAME/KEY: CDS
134 <222> LOCATION: (81)..(1718)
136 <400> SEQUENCE: 3
137 cggaaattccct ctactaacaa taccagatcc agtctagcgt ttcgatttc tgcttcacat 60
139 ttctgtttct ttgaccagaa atg gca atc gcg gct caa act ccg gac att ctc 113

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140	Met Ala Ile Ala Ala Gln Thr Pro Asp Ile Leu	
141	1 5 10	
143	ggc gaa cgt cag tcc ggc cag gac gtc cgc act caa aat gtg gtg gca	161
144	Gly Glu Arg Gln Ser Gly Gln Asp Val Arg Thr Gln Asn Val Val Ala	
145	15 20 25	
147	tgt caa gcg gtt gcc aat att gtc aaa tct tca ctt ggt cct gtc gga	209
148	Cys Gln Ala Val Ala Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly	
149	30 35 40	
151	ctc gac aag atg cta gtg gat att ggt gat gta aca att aca aat	257
152	Leu Asp Lys Met Leu Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn	
153	45 50 55	
155	gat ggt gct acg att ctt aag atg tta gaa gta gag cat cct gca gca	305
156	Asp Gly Ala Thr Ile Leu Lys Met Leu Glu Val Glu His Pro Ala Ala	
157	60 65 70 75	
159	aag gtg ctc gtg gag ttg gct gag ctt caa gac cga gaa gtt gga gat	353
160	Lys Val Leu Val Glu Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp	
161	80 85 90	
163	qga acc act tcg gtt gtc atc ata gca gct gag ttg ctc aag aga gca	401
164	Gly Thr Thr Ser Val Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala	
165	95 100 105	
167	aat gat ctc gtg agg aat aag atc cac cca aca tca ata atc agt gga	449
168	Asn Asp Leu Val Arg Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly	
169	110 115 120	
171	tac agg ctt gct atg agg gaa gca tgc aag tat gtt gaa gag aaa ttg	497
172	Tyr Arg Leu Ala Met Arg Glu Ala Cys Lys Tyr Val Glu Glu Lys Leu	
173	125 130 135	
175	tca atg aag gtt gaa aag ctt gga aaa gat tct cta gta aac tgt gca	545
176	Ser Met Lys Val Glu Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala	
177	140 145 150 155	
179	aag aca agc atg tcc tca aag ttg ata gct ggt gac agc gac ttc ttt	593
180	Lys Thr Ser Met Ser Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe	
181	160 165 170	
183	gca aat ttg gtt gta gat gct gta caa gca gta aag atg acc aat gca	641
184	Ala Asn Leu Val Val Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala	
185	175 180 185	
187	cgg ggg gaa atc aaa tat cct atc aag agt ata aat att ttg aaa gct	689
188	Arg Gly Glu Ile Lys Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala	
189	190 195 200	
191	cat gga aaa agt gca aga gat agc tgc ctt ttg aat ggc tat gct ctc	737
192	His Gly Lys Ser Ala Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu	
193	205 210 215	
195	aat act ggt cgt gct gca ggg atg cct atg aga gtt gca cct gca	785
196	Asn Thr Gly Arg Ala Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala	
197	220 225 230 235	
199	agg att gct tgt ctt gac ttt aat ctt cag aaa acg aag atg caa ttg	833
200	Arg Ile Ala Cys Leu Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu	
201	240 245 250	
203	ggt gta caa gtc tta gtc act gat ccc agg gag ctt gaa aga att cgt	881
204	Gly Val Gln Val Leu Val Thr Asp Pro Arg Glu Leu Glu Arg Ile Arg	

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205	255	260	265	
207	caa aga gaa gct gat atg aca aag gaa cgg att gag aaa ctc ctg aaa			929
208	Gln Arg Glu Ala Asp Met Thr Lys Glu Arg Ile Glu Lys Leu Leu Lys			
209	270	275	280	
211	gct gga gca aat gtt gtt cta acc aca aag gga att gat gac atg gca			977
212	Ala Gly Ala Asn Val Val Leu Thr Thr Lys Gly Ile Asp Asp Met Ala			
213	285	290	295	
215	ctt aaa tat ttt gtg gag gct ggg gct att gct gtg aga cgt gtt cgg			1025
216	Leu Lys Tyr Phe Val Glu Ala Gly Ala Ile Ala Val Arg Arg Val Arg			
217	300	305	310	315
219	aaa gag gat atg cgc cat gtt gcc aag gca act ggt gca aca ctg gtt			1073
220	Lys Glu Asp Met Arg His Val Ala Lys Ala Thr Gly Ala Thr Leu Val			
221	320	325	330	
223	tca aca ttt gct gac atg gaa gga gag gaa aca ttt gat tca tca ctg			1121
224	Ser Thr Phe Ala Asp Met Glu Gly Glu Glu Thr Phe Asp Ser Ser Leu			
225	335	340	345	
227	ctt gga caa gct gaa gaa gtt gtg gag gag cgc att gct gat gac gat			1169
228	Leu Gly Gln Ala Glu Glu Val Val Glu Glu Arg Ile Ala Asp Asp Asp			
229	350	355	360	
231	gtg att atg ata aaa ggg aca aag act aca agt gcg gtt tcc ttg att			1217
232	Val Ile Met Ile Lys Gly Thr Lys Thr Thr Ser Ala Val Ser Leu Ile			
233	365	370	375	
235	ctt cgt ggt gca aat gac tat atg ctc gat gag atg gag cga gcc ctg			1265
236	Leu Arg Gly Ala Asn Asp Tyr Met Leu Asp Glu Met Glu Arg Ala Leu			
237	380	385	390	395
239	cat gat gct tta tgt att gtc aag aga acc ctt gaa tct aat aca gta			1313
240	His Asp Ala Leu Cys Ile Val Lys Arg Thr Leu Glu Ser Asn Thr Val			
241	400	405	410	
243	gtt gca ggt gga ggt gct gtt gag gct gcc ttg tct gtg cac ttg gag			1361
244	Val Ala Gly Gly Ala Val Glu Ala Ala Leu Ser Val His Leu Glu			
245	415	420	425	
247	tac ctc gct aca act ctt ggg tca cga gag cag tta gca ata gca gag			1409
248	Tyr Leu Ala Thr Thr Leu Gly Ser Arg Glu Gln Leu Ala Ile Ala Glu			
249	430	435	440	
251	ttt gca gaa tcc ttg ttg att ata cca aag gtt ctt gct gtc aat gct			1457
252	Phe Ala Glu Ser Leu Leu Ile Ile Pro Lys Val Leu Ala Val Asn Ala			
253	445	450	455	
255	gcc aaa gat gcc act gaa tta gct gca aaa ctc cgg gct tac cac cat			1505
256	Ala Lys Asp Ala Thr Glu Leu Ala Ala Lys Leu Arg Ala Tyr His His			
257	460	465	470	475
259	aca gca caa aca aag gct gat aag aaa cat tta tca agc atg gga cta			1553
260	Thr Ala Gln Thr Lys Ala Asp Lys Lys His Leu Ser Ser Met Gly Leu			
261	480	485	490	
263	gac ctt tca aag ggg acc atc cga aac aac tta gaa gct gga gtc att			1601
264	Asp Leu Ser Lys Gly Thr Ile Arg Asn Asn Leu Glu Ala Gly Val Ile			
265	495	500	505	
267	gaa cct gca atg agc aaa ata aag ata att cag ttt gct act gaa gca			1649
268	Glu Pro Ala Met Ser Lys Ile Lys Ile Ile Gln Phe Ala Thr Glu Ala			
269	510	515	520	

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271 gcc ata aca att ctt cga att gat gac atg atc aag ctt gtc aag gat      1697
272 Ala Ile Thr Ile Leu Arg Ile Asp Asp Met Ile Lys Leu Val Lys Asp
273      525           530           535
275 gag act cag aat gaa gag gaa tagatgcaga ctcttctaag ctgcctccct      1748
276 Glu Thr Gln Asn Glu Glu Glu
277 540           545
279 ttgtttca aatttgtgtc ccttgcgagc tggaggaaag ggggggtgt tatgtggtgt 1808
281 tttcagtgtt ttaattttt caaggagctc gcggctgtg tacttttaggt tagagtccat 1868
283 ccaagggtgt tttattggat aatgcctaag ctgttctcg tctatttagta ggctggtagt 1928
285 tccactgagt tctcatccca attaaaagaa tgagatcaa gggctctaaa ttcgtactca 1988
287 ttggtgcacg atttgttct gacaaggata agacttgacc ctctctatca caataaaaaaa 2048
289 aaaaaaaaaa aa                                         2060
292 <210> SEQ ID NO: 4
293 <211> LENGTH: 546
294 <212> TYPE: PRT
295 <213> ORGANISM: Bruguiera sexangula
297 <400> SEQUENCE: 4
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301 Gly Gln Asp Val Arg Thr Gln Asn Val Val Ala Cys Gln Ala Val Ala
302      20          25          30
304 Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly Leu Asp Lys Met Leu
305      35          40          45
307 Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn Asp Gly Ala Thr Ile
308      50          55          60
310 Leu Lys Met Leu Glu Val Glu His Pro Ala Ala Lys Val Leu Val Glu
311      65          70          75          80
313 Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp Gly Thr Thr Ser Val
314      85          90          95
316 Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala Asn Asp Leu Val Arg
317      100         105         110
319 Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly Tyr Arg Leu Ala Met
320      115         120         125
322 Arg Glu Ala Cys Lys Tyr Val Glu Glu Lys Leu Ser Met Lys Val Glu
323      130         135         140
325 Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala Lys Thr Ser Met Ser
326 145           150         155         160
328 Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe Ala Asn Leu Val Val
329      165         170         175
331 Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala Arg Gly Glu Ile Lys
332      180         185         190
334 Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala His Gly Lys Ser Ala
335      195         200         205
337 Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu Asn Thr Gly Arg Ala
338      210         215         220
340 Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala Arg Ile Ala Cys Leu
341 225           230         235         240
343 Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu Gly Val Gln Val Leu
344      245         250         255

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date